

Table 3. MCSs containing clustered putative transcription factor-binding sites.

Potential binding sites for the indicated transcription factors were identified in three MCSs based on searching TRANSFAC 5.0 (Matys et al. 2003).

MCS Position ^a	No. Sites ^b	Total Sites ^c	Transcription Factor Name	p-value ^d	Location
534407-534960	5	60	STE11	0.0056	4 kb downstream of MET exon 2. (See Fig. 6)
	3	13	HFH2	0.0039	
	4	37	HFH3	0.068	
	2	10	P53	0.114	
508835-509106	3	15	MEF2	0.0062	6.2 kb downstream of MET exon 1
590100-590504	3	13	CCAAT	0.0039	1.1 kb downstream of MET exon 10
	3	26	CF1	0.032	

^aCoordinates within the human reference sequence of the targeted region, as displayed in the customized UCSC Genome Browser (see <http://genome.ucsc.edu>).

^bThe number of putative binding sites for each transcription factor in each MCS.

^cTotal number of putative sites in the ~1.8-Mb targeted region.

^dP-value reflecting the probability that there exists an MCS with at least as many clustered sites as that observed, assuming a uniform distribution (see Methods).

References

Matys, V., Fricke, E., Geffers, R., Gossling, E., Haubrock, M., Hehl, R., Hornischer, K., Karas, D., Kel, A.E., Kel-Margoulis, O.V. et al. 2003. TRANSFAC: transcriptional regulation, from patterns to profiles. *Nucleic Acids Res* **31**: 374-378.